

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, SCISEARCH' ENTERED AT 18:25:59 ON  
21 JUN 2006

```
L1      2 SEA ABB=ON  PLU=ON  CAPSULATUM (20W) (CHITIN (2W) SYNTHASE)
L2      2 DUP REM L1 (0 DUPLICATES REMOVED)
        D L2 BIB ABS 1-2
L3      2949 SEA ABB=ON  PLU=ON  (CHITIN (2W) SYNTHASE)
L4      14 SEA ABB=ON  PLU=ON  L3 AND CAPSULATUM
L5      14 DUP REM L4 (0 DUPLICATES REMOVED)
        D L5 BIB ABS 1-14
L6      28165 SEA ABB=ON  PLU=ON  JOHNSON C?/AU
L7      23 SEA ABB=ON  PLU=ON  L6 AND CAPSULATUM
L8      11 DUP REM L7 (12 DUPLICATES REMOVED)
        D L8 BIB ABS 1-11
L9      0 SEA ABB=ON  PLU=ON  MCEMEN J?/AU
L10     1456 SEA ABB=ON  PLU=ON  MCEWEN J?/AU
L11     37 SEA ABB=ON  PLU=ON  L10 AND CAPSULATUM
L12     16 DUP REM L11 (21 DUPLICATES REMOVED)
        D L12 BIB ABS 1-16
```

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	4489	johnson-c\$.in. mcewen-j\$.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/21 18:35
L2	3	1 and capsulatum	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/21 18:35
L3	271	chitin near2 synthase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/21 18:36
L4	40	3 and capsulatum	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/21 18:36
L5	1	3 same capsulatum	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/21 18:36

GenCore version 5.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 04:36:41 ; Search time 2622.09 Seconds  
 (without alignments)  
 6853.025 Million cell updates/sec

Title: US-10-718-955-1  
 Perfect score: 281  
 Sequence: 1 gtgagaaaacactctttcct.....tgccccttaaatacgctccag 281

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

Database : GenEmbl:\*  
 1: gb\_env:\*  
 2: gb\_pat:\*  
 3: gb\_ph:\*  
 4: gb\_pl:\*  
 5: gb\_pr:\*  
 6: gb\_ro:\*  
 7: gb\_sts:\*  
 8: gb\_sy:\*  
 9: gb\_un:\*  
 10: gb\_vi:\*  
 11: gb\_ov:\*  
 12: gb\_htg:\*  
 13: gb\_in:\*  
 14: gb\_om:\*  
 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	83.6	29.8	92585	12	CT033796	CT033796 Danio rer
c	2	82.8	29.5	362	13	AF359997	AF359997 Penaeus (
	3	82.2	29.3	162768	12	AC148720	AC148720 Ictalurus
	4	81.4	29.0	216720	12	AC112768	AC112768 Rattus no
	5	81.2	28.9	185946	11	BX548045	BX548045 Zebrafish
c	6	81	28.8	158797	12	CR854915	CR854915 Danio rer
c	7	81	28.8	179729	11	BX530035	BX530035 Zebrafish

	8	81	28.8	183364	12	CR933838	CR933838	Danio rer
	9	80.8	28.8	200882	11	AL953852	AL953852	Zebrafish
c	10	80.6	28.7	245423	12	AC131848	AC131848	Rattus no
c	11	80.2	28.5	64433	12	AC131600	AC131600	Mus muscu
c	12	80.2	28.5	192484	6	AC134906	AC134906	Mus muscu
c	13	80.2	28.5	195273	6	AC147474	AC147474	Mus muscu
c	14	79.8	28.4	174999	11	AL840636	AL840636	Zebrafish
c	15	79.8	28.4	175342	11	AL807799	AL807799	Zebrafish
	16	79.8	28.4	210873	12	CR391917	CR391917	Danio rer
	17	79.8	28.4	222137	12	CR954958	CR954958	Danio rer
	18	79.6	28.3	170260	11	BX908763	BX908763	Zebrafish
c	19	79.6	28.3	204103	11	BX088705	BX088705	Zebrafish
	20	79.6	28.3	258612	12	AC095939	AC095939	Rattus no
c	21	79.4	28.3	155228	6	AC134399	AC134399	Mus muscu
c	22	79.4	28.3	164878	12	CT025582	CT025582	Danio rer
	23	79.4	28.3	177877	6	AC163995	AC163995	Mus muscu
c	24	79.4	28.3	194427	6	AC165080	AC165080	Mus muscu
c	25	79.4	28.3	203399	12	AC121559	AC121559	Mus muscu
c	26	79.4	28.3	204468	12	AC165354	AC165354	Mus muscu
c	27	79.2	28.2	144823	11	BX897744	BX897744	Zebrafish
	28	79.2	28.2	152517	11	BX927074	BX927074	Zebrafish
	29	79.2	28.2	196336	11	BX572621	BX572621	Zebrafish
	30	79.2	28.2	261898	12	CR926458	CR926458	Danio rer
	31	79.2	28.2	349980	2	CQ870290	CQ870290	Sequence
	32	79	28.1	142743	6	AL645695	AL645695	Mouse DNA
c	33	79	28.1	192579	12	AC141584	AC141584	Rattus no
	34	79	28.1	209713	12	CT027692	CT027692	Danio rer
c	35	78.8	28.0	85185	11	BX322638	BX322638	Zebrafish
	36	78.8	28.0	110000	4	AP008211_190	Continuation (191	
	37	78.8	28.0	136195	11	BX465849	BX465849	Zebrafish
	38	78.8	28.0	143739	4	AC132483	AC132483	Oryza sat
	39	78.8	28.0	160405	11	BX510999	BX510999	Zebrafish
	40	78.8	28.0	161346	11	BX511013	BX511013	Zebrafish
c	41	78.8	28.0	192541	6	AC153502	AC153502	Mus muscu
c	42	78.6	28.0	115973	12	CT573113	CT573113	Danio rer
	43	78.6	28.0	149928	12	AC134950	AC134950	Danio rer
c	44	78.6	28.0	154856	12	AC119792	AC119792	Rattus no
c	45	78.6	28.0	156284	11	AL929336	AL929336	Zebrafish
c	46	78.6	28.0	179154	12	AC141487	AC141487	Rattus no
	47	78.6	28.0	188859	11	BX247903	BX247903	Zebrafish
c	48	78.6	28.0	192603	11	BX323087	BX323087	Zebrafish
	49	78.6	28.0	196462	12	CT025856	CT025856	Danio rer
c	50	78.6	28.0	203466	6	AC162920	AC162920	Mus muscu
c	51	78.4	27.9	162206	12	CR926911	CR926911	Danio rer
c	52	78.4	27.9	241995	12	AC097900	AC097900	Rattus no
	53	78.4	27.9	245166	12	AC107262	AC107262	Rattus no
	54	78.2	27.8	120558	11	CR450689	CR450689	Zebrafish
	55	78.2	27.8	186106	12	BX088565	BX088565	Danio rer
c	56	78.2	27.8	186318	11	BX119930	BX119930	Zebrafish
c	57	78.2	27.8	191281	11	AL935185	AL935185	Zebrafish
c	58	78.2	27.8	191781	11	BX000480	BX000480	Zebrafish
	59	78.2	27.8	204383	12	CR854910	CR854910	Danio rer
	60	78.2	27.8	232104	11	CR457452	CR457452	Zebrafish
c	61	78	27.8	122188	12	CT009763	CT009763	Danio rer
	62	78	27.8	129787	12	CR926460	CR926460	Danio rer
c	63	78	27.8	144640	11	CR847530	CR847530	Zebrafish
c	64	78	27.8	145320	11	CR381553	CR381553	Zebrafish
	65	78	27.8	154419	11	BX957287	BX957287	Zebrafish
	66	78	27.8	155366	11	BX294662	BX294662	Zebrafish
c	67	78	27.8	170622	12	CR932359	CR932359	Danio rer
c	68	78	27.8	171493	11	BX649575	BX649575	Zebrafish

c	69	78	27.8	174986	11	AL935126	AL935126 Zebrafish
	70	78	27.8	177516	11	BX294164	BX294164 Zebrafish
	71	78	27.8	180836	12	CR925859	CR925859 Danio rer
	72	78	27.8	183380	11	BX469930	BX469930 Zebrafish
	73	78	27.8	186123	11	BX640592	BX640592 Zebrafish
c	74	78	27.8	189108	6	AC119242	AC119242 Mus muscu
	75	78	27.8	198900	11	BX470185	BX470185 Zebrafish
	76	78	27.8	202348	6	AC154308	AC154308 Mus muscu
c	77	78	27.8	206857	6	AC152959	AC152959 Mus muscu
	78	78	27.8	209195	11	AL954309	AL954309 Zebrafish
c	79	78	27.8	216418	12	CR354597	CR354597 Danio rer
c	80	78	27.8	230233	6	CT009702	CT009702 Mouse DNA
	81	78	27.8	311860	12	BX537353	BX537353 Danio rer
	82	77.8	27.7	138341	11	AL935053	AL935053 Zebrafish
c	83	77.8	27.7	174828	11	CR352326	CR352326 Zebrafish
c	84	77.8	27.7	264976	12	AC132800	AC132800 Rattus no
	85	77.6	27.6	154017	11	CR774185	CR774185 Zebrafish
c	86	77.6	27.6	162570	11	BX927311	BX927311 Zebrafish
c	87	77.6	27.6	167004	11	AL954840	AL954840 Zebrafish
	88	77.6	27.6	189417	6	BX000995	BX000995 Mouse DNA
c	89	77.6	27.6	201139	12	AC110548	AC110548 Mus muscu
	90	77.6	27.6	202346	6	AC121523	AC121523 Mus muscu
	91	77.4	27.5	140087	12	CR931815	CR931815 Danio rer
c	92	77.4	27.5	172954	11	AL929152	AL929152 Zebrafish
	93	77.4	27.5	190385	12	CT573411	CT573411 Danio rer
	94	77.4	27.5	236418	12	CR318626	CR318626 Danio rer
c	95	77.2	27.5	47439	11	BX901875	BX901875 Zebrafish
c	96	77.2	27.5	139220	11	CR936460	CR936460 Zebrafish
	97	77.2	27.5	141291	6	AC157092	AC157092 Mus muscu
	98	77.2	27.5	208710	6	AC118200	AC118200 Mus muscu
	99	77.2	27.5	222615	12	AC121379	AC121379 Rattus no

GenCore version 5.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 04:26:31 ; Search time 945.656 Seconds  
 (without alignments)  
 2071.790 Million cell updates/sec

Title: US-10-718-955-1  
 Perfect score: 281  
 Sequence: 1 gtgagaaaacactctttcct.....tgccccttaaatacgctccag 281

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

Database : N\_Geneseq\_8:\*  
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 2: geneseqn1990s:\*  
 3: geneseqn2000s:\*  
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 10: geneseqn2003cs:\*  
 11: geneseqn2003ds:\*  
 12: geneseqn2004as:\*  
 13: geneseqn2004bs:\*  
 14: geneseqn2005s:\*  
 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	82.8	29.5	926	3	ABN81102	Abn81102 Shrimp po
	2	79.2	28.2	110000	13	ABD32966_02	Continuation (3 of
c	3	78.6	28.0	261066	14	AEE04993	Aee04993 Cancer-as
	4	71.8	25.6	111206	11	ACN45152	Acn45152 Mouse gen
	5	71.2	25.3	242496	14	AED76150	Aed76150 Mouse CA
	6	70.6	25.1	138627	12	ADQ97183	Adq97183 Human can
	7	70.2	25.0	110000	15	AEF10213_0	Aef10213 Human pro

	8	70.2	25.0	260160	12	ADQ20017	Adq20017 Human sof
	9	69.4	24.7	70215	11	ACN43992	Acn43992 Mouse gen
	10	68.8	24.5	235962	14	ADZ12926	Adz12926 Murine ca
c	11	67.6	24.1	46456	9	ADA02825	Ada02825 Mouse Pou
c	12	67.6	24.1	46456	10	ADB72563	Adb72563 Mouse Pou
c	13	67.6	24.1	46456	12	ADM74420	Adm74420 Murine ca
c	14	67.6	24.1	46458	10	ADC85304	Adc85304 Human Sos
c	15	67.2	23.9	96599	9	ADA02747	Ada02747 Mouse Irf
c	16	67.2	23.9	96599	10	ADB72485	Adb72485 Mouse Irf
c	17	67.2	23.9	96599	10	ADC85227	Adc85227 Mouse Irf
c	18	67.2	23.9	96599	12	ADM74342	Adm74342 Murine ca
	19	65.6	23.3	261817	11	ACN45182	Acn45182 Human gen
	20	64.4	22.9	31277	11	ACN44854	Acn44854 Human gen
c	21	64.4	22.9	126488	14	ADZ12943	Adz12943 Human can
	22	64	22.8	123192	13	ADV34995	Adv34995 Murine cD
	23	64	22.8	155350	13	ABD33514	Abd33514 Murine ca
	24	63.8	22.7	134000	14	AED76160	Aed76160 Mouse CA
	25	63.6	22.6	54810	13	ABD32759	Abd32759 Mouse can
	26	63.6	22.6	79544	12	ADQ97764	Adq97764 Human can
c	27	63.2	22.5	198522	11	ACN44010	Acn44010 Human gen
	28	63	22.4	2983	4	AAK83652	Aak83652 Human imm
	29	63	22.4	15698	6	ABL34141	Abl34141 Human imm
c	30	63	22.4	89824	13	ABD32895	Abd32895 Mouse can
	31	62.8	22.3	256493	11	ACN44514	Acn44514 Human gen
c	32	62.6	22.3	42611	10	ABV75791	Abv75791 Human lip
c	33	62.6	22.3	43672	11	ACN44252	Acn44252 Mouse gen
	34	62.6	22.3	117962	8	AAD54480	Aad54480 Human CIP
	35	62.6	22.3	227968	6	ABK83497	Abk83497 Human cDN
	36	62.6	22.3	227968	12	ADQ18538	Adq18538 Human sof
	37	62.6	22.3	227968	14	AED17856	Aed17856 Fibrotic
c	38	62.4	22.2	196063	13	ABD33462	Abd33462 Human can
c	39	61.8	22.0	141463	11	ACN43862	Acn43862 Human gen
	40	61.4	21.9	87468	15	AEF10213_3	Continuation (4 of
	41	61	21.7	2889	4	AAK83654	Aak83654 Human imm
	42	61	21.7	6727	2	AAT88014	Aat88014 Murine IL
	43	61	21.7	6727	3	AAC73648	Aac73648 Murine IL
	44	61	21.7	6727	8	ABX04302	Abx04302 Mouse Int
	45	61	21.7	6727	12	ADR11979	Adr11979 Murine in
c	46	61	21.7	11112	6	ABQ72905	Abq72905 Human GRM
c	47	61	21.7	11112	6	ABQ72798	Abq72798 Human GRM
	48	61	21.7	48133	11	ACN44860	Acn44860 Mouse gen
c	49	60.8	21.6	36221	10	ADH63075	Adh63075 Human fib
	50	60.8	21.6	110000	12	ADQ97050_2	Continuation (3 of
c	51	60.6	21.6	7576	12	ADM67662	Adm67662 Rice Ehd1
	52	60.6	21.6	210528	11	ACN44040	Acn44040 Mouse gen
	53	60.4	21.5	26997	4	AAS46748	Aas46748 Tumour su
c	54	60.2	21.4	110000	13	ABD32966_07	Continuation (8 of
c	55	60	21.4	110000	13	ABD32966_06	Continuation (7 of
	56	59.8	21.3	1807	13	ADR07494	Adr07494 Full leng
c	57	59.8	21.3	110000	12	ADN97989_13	Continuation (14 o
	58	59.8	21.3	110000	14	ADZ46976_0	Adz46976 Human pho
c	59	59.8	21.3	304326	13	ADS15253	Ads15253 Rat senso
	60	59.6	21.2	6621	6	ABK33932	Abk33932 Human DNA
	61	59.6	21.2	6621	6	ABL70155	Abl70155 Chemicall
	62	59.6	21.2	6621	6	AAS61097	Aas61097 Human gen
	63	59.6	21.2	6621	8	ABZ09983	Abz09983 Haematopo
	64	59.6	21.2	6621	8	ABZ10129	Abz10129 Haematopo
	65	59.6	21.2	6621	8	ABZ10097	Abz10097 Haematopo
	66	59.6	21.2	6621	8	ABZ10243	Abz10243 Haematopo
	67	59.6	21.2	6621	8	ADA20344	Ada20344 Prostate
	68	59.6	21.2	6621	8	ADA84151	Ada84151 Human ren

	69	59.6	21.2	6621	10	ADE84153	Ade84153 Human lym
	70	59.6	21.2	6621	10	ADE84077	Ade84077 Human lym
c	71	59.6	21.2	7204	2	AAX23527	Aax23527 O. longis
c	72	59.6	21.2	104932	14	AEB96542	Aeb96542 Human STA
c	73	59.6	21.2	110000	14	AED76254_06	Continuation (7 of
c	74	59.4	21.1	3442	10	ADB58100	Adb58100 Toxicity-
	75	59.4	21.1	11745	6	ABK28331	Abk28331 DNA trans
c	76	59.2	21.1	110021	13	ABD32859	Abd32859 Mouse can
	77	59.2	21.1	119057	13	ABD33460	Abd33460 Murine ca
c	78	59.2	21.1	219715	13	ABD32692	Abd32692 Mouse can
	79	59	21.0	2551	2	AAT30738	Aat30738 Rat crypt
c	80	59	21.0	4559	4	AAH27886	Aah27886 Nucleotid
	81	59	21.0	12069	6	ABK39931	Abk39931 Human che
	82	59	21.0	32185	11	ACN44604	Acn44604 Mouse gen
	83	59	21.0	289106	14	ADZ12614	Adz12614 Murine ca
	84	59	21.0	326014	6	ABK89296	Abk89296 Human gen
	85	59	21.0	326014	12	ADQ94981	Adq94981 Human kin
c	86	58.8	20.9	3354	14	ADZ70903	Adz70903 Human mat
	87	58.8	20.9	22461	14	AED76280	Aed76280 Mouse CA
	88	58.8	20.9	135652	14	AEE05069	Aee05069 Cancer-as
c	89	58.6	20.9	13217	4	AAS35088	Aas35088 DNA #38 e
	90	58.6	20.9	13217	4	AAS31477	Aas31477 Human DNA
c	91	58.6	20.9	13217	4	AAI63997	Aai63997 Human pol
c	92	58.6	20.9	13217	4	ABA06818	Aba06818 Human gen
c	93	58.6	20.9	13217	5	ABA18587	Aba18587 Human ner
c	94	58.6	20.9	13217	5	AAS29749	Aas29749 Human end
	95	58.6	20.9	13217	6	ABQ66801	Abq66801 Human pol
c	96	58.6	20.9	13217	6	ABV84155	Abv84155 Human pol
	97	58.6	20.9	13217	10	ADC11088	Adc11088 Human DNA
c	98	58.6	20.9	13217	10	ADC46530	Adc46530 Human neo
c	99	58.6	20.9	13217	12	ADM24712	Adm24712 Human PRO

GenCore version 5.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 04:56:26 ; Search time 268.82 Seconds  
 (without alignments)  
 1955.884 Million cell updates/sec

Title: US-10-718-955-1  
 Perfect score: 281  
 Sequence: 1 gtgagaaaacactctttcct.....tgccccttaaatacgctccag 281

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

Database : Issued\_Patents\_NA:\*  
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 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	65.6	23.3	194937	3	US-09-949-016-17032	Sequence 17032, A
2	65.6	23.3	194937	3	US-09-949-016-17033	Sequence 17033, A
c 3	65.4	23.3	601	3	US-09-949-016-198482	Sequence 198482,
c 4	64.2	22.8	601	3	US-09-949-016-198483	Sequence 198483,
c 5	64.2	22.8	601	3	US-09-949-016-198484	Sequence 198484,
6	64.2	22.8	767677	3	US-09-949-016-12147	Sequence 12147, A
7	64.2	22.8	767677	3	US-09-949-016-17361	Sequence 17361, A
c 8	63.8	22.7	601	3	US-09-949-016-198480	Sequence 198480,
c 9	63.8	22.7	601	3	US-09-949-016-198481	Sequence 198481,
c 10	63.4	22.6	16434	3	US-09-949-016-13235	Sequence 13235, A
c 11	63.4	22.6	26831	3	US-09-949-016-16250	Sequence 16250, A
12	61	21.7	6727	3	US-08-629-643A-5	Sequence 5, Appli

	13	61	21.7	6727	3	US-09-280-799-1	Sequence 1, Appli
	14	61	21.7	6727	3	US-09-155-884-5	Sequence 5, Appli
c	15	60.8	21.6	36221	3	US-09-954-556-29	Sequence 29, Appl
	16	60.8	21.6	670689	3	US-09-949-016-12505	Sequence 12505, A
	17	60.8	21.6	670690	3	US-09-949-016-14207	Sequence 14207, A
	18	59.4	21.1	112114	3	US-09-949-016-17292	Sequence 17292, A
	19	59.4	21.1	154605	3	US-09-949-016-11894	Sequence 11894, A
	20	59	21.0	2551	2	US-08-486-013-70	Sequence 70, Appl
	21	59	21.0	2551	2	US-08-482-279-70	Sequence 70, Appl
	22	59	21.0	2551	2	US-08-342-268-70	Sequence 70, Appl
	23	59	21.0	2551	3	US-09-015-968-70	Sequence 70, Appl
	24	59	21.0	2551	3	US-09-397-386-70	Sequence 70, Appl
c	25	58.2	20.7	12645	3	US-09-949-016-12306	Sequence 12306, A
	26	58	20.6	601	3	US-09-949-016-57873	Sequence 57873, A
	27	58	20.6	72048	3	US-09-949-002-600	Sequence 600, App
	28	58	20.6	72048	3	US-09-949-002-684	Sequence 684, App
	29	57.6	20.5	601	3	US-09-949-002-5378	Sequence 5378, Ap
	30	57.4	20.4	87648	3	US-09-949-016-13655	Sequence 13655, A
	31	57.2	20.4	304533	3	US-09-949-016-15371	Sequence 15371, A
	32	57.2	20.4	304533	3	US-09-949-016-15372	Sequence 15372, A
	33	57	20.3	601	3	US-09-949-016-31837	Sequence 31837, A
	34	57	20.3	601	3	US-09-949-016-40022	Sequence 40022, A
	35	57	20.3	601	3	US-09-949-016-74004	Sequence 74004, A
	36	57	20.3	601	3	US-09-949-016-74110	Sequence 74110, A
	37	57	20.3	1016	2	US-08-109-391A-3	Sequence 3, Appli
	38	57	20.3	1016	2	US-08-459-019A-3	Sequence 3, Appli
	39	57	20.3	1016	2	US-08-460-428A-3	Sequence 3, Appli
	40	57	20.3	1016	3	US-08-458-860A-3	Sequence 3, Appli
	41	57	20.3	1016	3	US-09-196-447B-3	Sequence 3, Appli
c	42	57	20.3	69813	3	US-09-949-016-12455	Sequence 12455, A
c	43	57	20.3	69813	3	US-09-949-016-13905	Sequence 13905, A
c	44	57	20.3	69813	3	US-09-949-016-13906	Sequence 13906, A
c	45	57	20.3	69833	3	US-09-949-016-12861	Sequence 12861, A
	46	56.8	20.2	601	3	US-09-949-016-57872	Sequence 57872, A
	47	56.8	20.2	236474	3	US-09-949-016-13418	Sequence 13418, A
c	48	56.6	20.1	4084	3	US-08-866-340-1	Sequence 1, Appli
c	49	56.6	20.1	4460	3	US-09-103-875-4	Sequence 4, Appli
	50	56.4	20.1	601	3	US-09-949-002-5377	Sequence 5377, Ap
	51	56.4	20.1	23015	3	US-09-949-002-726	Sequence 726, App
	52	56.2	20.0	601	3	US-09-949-016-21200	Sequence 21200, A
	53	56.2	20.0	601	3	US-09-949-016-158641	Sequence 158641,
c	54	56.2	20.0	601	3	US-09-949-002-1427	Sequence 1427, Ap
c	55	56.2	20.0	601	3	US-09-949-002-4680	Sequence 4680, Ap
	56	56.2	20.0	35688	3	US-09-949-016-16873	Sequence 16873, A
c	57	56.2	20.0	41431	3	US-09-949-016-11908	Sequence 11908, A
c	58	56.2	20.0	41433	3	US-09-949-016-16176	Sequence 16176, A
c	59	56	19.9	144158	3	US-09-949-016-11755	Sequence 11755, A
c	60	56	19.9	144158	3	US-09-949-016-12936	Sequence 12936, A
	61	55.8	19.9	4072	3	US-09-272-496-7	Sequence 7, Appli
c	62	55.8	19.9	129127	3	US-09-949-016-13481	Sequence 13481, A
c	63	55.6	19.8	27067	3	US-09-841-158-5	Sequence 5, Appli
	64	55.6	19.8	71863	3	US-09-949-016-15112	Sequence 15112, A
	65	55.6	19.8	421118	3	US-09-949-016-16297	Sequence 16297, A
c	66	55.4	19.7	601	3	US-09-949-016-21199	Sequence 21199, A
c	67	55.4	19.7	601	3	US-09-949-016-21200	Sequence 21200, A
c	68	55.4	19.7	601	3	US-09-949-016-158640	Sequence 158640,
c	69	55.4	19.7	601	3	US-09-949-016-158641	Sequence 158641,
	70	55.4	19.7	41431	3	US-09-949-016-11908	Sequence 11908, A
	71	55.4	19.7	41433	3	US-09-949-016-16176	Sequence 16176, A
c	72	55.4	19.7	68173	3	US-09-949-016-14046	Sequence 14046, A
	73	55.4	19.7	236964	3	US-09-949-016-15753	Sequence 15753, A

	74	55.2	19.6	601	3	US-09-949-016-85630	Sequence 85630, A
	75	55.2	19.6	340380	3	US-09-949-016-14179	Sequence 14179, A
	76	55	19.6	106924	3	US-09-949-016-13834	Sequence 13834, A
	77	54.8	19.5	601	3	US-09-949-002-5379	Sequence 5379, Ap
	78	54.8	19.5	37269	3	US-09-949-016-16672	Sequence 16672, A
	79	54.8	19.5	69813	3	US-09-949-016-12455	Sequence 12455, A
	80	54.8	19.5	69813	3	US-09-949-016-13905	Sequence 13905, A
	81	54.8	19.5	69813	3	US-09-949-016-13906	Sequence 13906, A
	82	54.8	19.5	69833	3	US-09-949-016-12861	Sequence 12861, A
	83	54.8	19.5	121049	3	US-09-949-016-17513	Sequence 17513, A
	84	54.6	19.4	2780	3	US-09-270-767-14877	Sequence 14877, A
c	85	54.6	19.4	13518	3	US-09-949-016-16687	Sequence 16687, A
c	86	54.6	19.4	15101	3	US-09-949-016-16974	Sequence 16974, A
c	87	54.6	19.4	41863	3	US-09-949-016-14948	Sequence 14948, A
	88	54.6	19.4	51589	3	US-09-949-016-16936	Sequence 16936, A
c	89	54.6	19.4	81335	3	US-09-949-002-709	Sequence 709, App
c	90	54.6	19.4	83707	3	US-09-949-002-595	Sequence 595, App
c	91	54.6	19.4	142504	3	US-09-949-016-13693	Sequence 13693, A
c	92	54.6	19.4	142506	3	US-09-949-016-12474	Sequence 12474, A
c	93	54.4	19.4	93778	3	US-09-949-016-15096	Sequence 15096, A
	94	54.4	19.4	312470	3	US-09-949-016-14043	Sequence 14043, A
	95	54.4	19.4	336024	3	US-09-949-016-12373	Sequence 12373, A
c	96	54.2	19.3	601	3	US-09-949-016-174857	Sequence 174857,
	97	54.2	19.3	3001	3	US-09-539-333D-215	Sequence 215, App
c	98	54.2	19.3	42479	3	US-09-949-016-16631	Sequence 16631, A
c	99	54.2	19.3	42479	3	US-09-949-016-16632	Sequence 16632, A
c	100	54.2	19.3	52202	3	US-09-949-016-17006	Sequence 17006, A

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 05:16:51 ; Search time 1776.48 Seconds  
 (without alignments)  
 1943.637 Million cell updates/sec

Title: US-10-718-955-1  
 Perfect score: 281  
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Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

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Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

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c	1	74.8	26.6	446	8	US-10-437-963-13776	Sequence 13776, A
	2	71.8	25.6	111206	6	US-10-087-192-1957	Sequence 1957, Ap
c	3	71.6	25.5	59247	8	US-10-741-601-5741	Sequence 5741, Ap
c	4	71.6	25.5	59247	9	US-10-741-600-17890	Sequence 17890, A
	5	71.6	25.5	161700	8	US-10-741-601-5623	Sequence 5623, Ap
	6	71.6	25.5	161700	9	US-10-741-600-17590	Sequence 17590, A

7	71	25.3	535	4	US-09-925-065A-40356	Sequence 40356, A
8	71	25.3	535	5	US-09-925-065A-40356	Sequence 40356, A
9	71	25.3	535	12	US-10-301-480-141594	Sequence 141594,
10	71	25.3	535	12	US-10-301-480-755003	Sequence 755003,
11	70.6	25.1	138627	11	US-10-330-773-159	Sequence 159, App
12	70.2	25.0	413	6	US-10-027-632-143335	Sequence 143335,
13	70.2	25.0	413	7	US-10-027-632-143335	Sequence 143335,
14	70.2	25.0	260160	9	US-10-723-860-2837	Sequence 2837, Ap
c 15	70	24.9	862	12	US-10-301-480-576730	Sequence 576730,
c 16	70	24.9	862	12	US-10-301-480-1190139	Sequence 1190139,
c 17	70	24.9	900	12	US-10-301-480-576729	Sequence 576729,
c 18	70	24.9	900	12	US-10-301-480-1190138	Sequence 1190138,
c 19	70	24.9	940	12	US-10-301-480-576728	Sequence 576728,
c 20	70	24.9	940	12	US-10-301-480-1190137	Sequence 1190137,
21	70	24.9	1048	4	US-09-925-065A-671970	Sequence 671970,
22	70	24.9	1048	4	US-09-925-065A-671971	Sequence 671971,
23	70	24.9	1048	4	US-09-925-065A-671972	Sequence 671972,
24	70	24.9	1048	4	US-09-925-065A-671973	Sequence 671973,
25	70	24.9	1048	5	US-09-925-065A-671970	Sequence 671970,
26	70	24.9	1048	5	US-09-925-065A-671971	Sequence 671971,
27	70	24.9	1048	5	US-09-925-065A-671972	Sequence 671972,
28	70	24.9	1048	5	US-09-925-065A-671973	Sequence 671973,
29	69.8	24.8	474	9	US-10-674-124A-18584	Sequence 18584, A
30	69.4	24.7	70215	6	US-10-087-192-217	Sequence 217, App
31	69.2	24.6	255	9	US-10-674-124A-26788	Sequence 26788, A
32	68.8	24.5	649	6	US-10-027-632-132892	Sequence 132892,
33	68.8	24.5	649	7	US-10-027-632-132892	Sequence 132892,
c 34	68.4	24.3	164	9	US-10-674-124A-12964	Sequence 12964, A
c 35	68	24.2	522	8	US-10-437-963-70393	Sequence 70393, A
c 36	68	24.2	536	8	US-10-437-963-74796	Sequence 74796, A
37	68	24.2	612	8	US-10-437-963-62485	Sequence 62485, A
c 38	67.6	24.1	509	8	US-10-437-963-67629	Sequence 67629, A
c 39	67.6	24.1	565	8	US-10-437-963-71038	Sequence 71038, A
c 40	67.6	24.1	688	12	US-10-301-480-576371	Sequence 576371,
c 41	67.6	24.1	688	12	US-10-301-480-1189780	Sequence 1189780,
c 42	67.6	24.1	46456	3	US-09-997-722-91	Sequence 91, Appl
c 43	67.4	24.0	1717	4	US-09-925-065A-682174	Sequence 682174,
c 44	67.4	24.0	1717	5	US-09-925-065A-682174	Sequence 682174,
c 45	67.2	23.9	96599	3	US-09-997-722-13	Sequence 13, Appl
46	66.8	23.8	510	8	US-10-437-963-56512	Sequence 56512, A
c 47	66.2	23.6	638	4	US-09-925-065A-72475	Sequence 72475, A
c 48	66.2	23.6	638	5	US-09-925-065A-72475	Sequence 72475, A
c 49	66.2	23.6	638	12	US-10-301-480-173714	Sequence 173714,
c 50	66.2	23.6	638	12	US-10-301-480-787123	Sequence 787123,

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 05:18:23 ; Search time 53.9381 Seconds  
 (without alignments)  
 588.091 Million cell updates/sec

Title: US-10-718-955-1  
 Perfect score: 281  
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Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

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Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
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1	50.2	17.9	2798	7	US-11-145-307A-179	Sequence 179, App
2	49	17.4	506	6	US-10-488-619-2562	Sequence 2562, Ap
3	48.8	17.4	2522	7	US-11-293-697-543	Sequence 543, App
c 4	46.2	16.4	2333	7	US-11-293-697-2386	Sequence 2386, Ap
5	44.2	15.7	3229	7	US-11-293-697-817	Sequence 817, App
6	43.6	15.5	42999	7	US-11-284-877-17	Sequence 17, Appl
c 7	43.2	15.4	1235	6	US-10-953-349-16337	Sequence 16337, A
8	43.2	15.4	151830	6	US-10-519-335-37	Sequence 37, Appl
c 9	41.8	14.9	2856	7	US-11-293-697-1116	Sequence 1116, Ap
10	41.6	14.8	6243	6	US-10-518-039-2	Sequence 2, Appli
11	41.6	14.8	6843	6	US-10-518-039-1	Sequence 1, Appli
12	41.6	14.8	394191	6	US-10-506-549-3	Sequence 3, Appli
13	41.4	14.7	342	7	US-11-217-529-80228	Sequence 80228, A
14	40	14.2	1235	6	US-10-953-349-16337	Sequence 16337, A

15	40	14.2	3335	7	US-11-293-697-1050	Sequence 1050, Ap
16	40	14.2	70665	6	US-10-505-928-596	Sequence 596, App
17	39.8	14.2	2523	7	US-11-293-697-1322	Sequence 1322, Ap
c 18	38.8	13.8	50000	6	US-10-528-659-2	Sequence 2, Appli
19	38.6	13.7	1989	7	US-11-293-697-362	Sequence 362, App
c 20	38.6	13.7	2307	7	US-11-293-697-1429	Sequence 1429, Ap
21	38.4	13.7	1174	6	US-10-953-349-2820	Sequence 2820, Ap
c 22	38.2	13.6	2567	6	US-10-196-749-179	Sequence 179, App
c 23	38	13.5	857	6	US-10-953-349-32928	Sequence 32928, A
24	37.6	13.4	534	6	US-10-505-928-2	Sequence 2, Appli
c 25	37.6	13.4	1733	7	US-11-293-697-1577	Sequence 1577, Ap
c 26	37.4	13.3	54550	7	US-11-318-813-42	Sequence 42, Appl
27	36.8	13.1	1538	6	US-10-953-349-17700	Sequence 17700, A
28	36.6	13.0	658	6	US-10-511-937-570	Sequence 570, App
c 29	36.6	13.0	1538	6	US-10-953-349-17700	Sequence 17700, A
c 30	36.6	13.0	1623	7	US-11-274-768A-1	Sequence 1, Appli
31	36.2	12.9	1631	7	US-11-293-697-1928	Sequence 1928, Ap
32	36.2	12.9	2460	7	US-11-293-697-595	Sequence 595, App
c 33	36.2	12.9	70665	6	US-10-505-928-596	Sequence 596, App
c 34	36.2	12.9	128361	6	US-10-505-928-151	Sequence 151, App
35	36.2	12.9	135090	6	US-10-505-928-607	Sequence 607, App
c 36	36	12.8	381	7	US-11-217-529-166545	Sequence 166545,
c 37	36	12.8	543	6	US-10-488-619-2662	Sequence 2662, Ap
38	36	12.8	2638	6	US-10-473-173-82	Sequence 82, Appl
c 39	36	12.8	2798	7	US-11-145-307A-179	Sequence 179, App
40	35.8	12.7	2025	6	US-10-511-937-414	Sequence 414, App
41	35.8	12.7	2681	7	US-11-145-307A-194	Sequence 194, App
c 42	35.8	12.7	135090	6	US-10-505-928-607	Sequence 607, App
c 43	35.8	12.7	151830	6	US-10-519-335-37	Sequence 37, Appl
44	35.6	12.7	857	6	US-10-953-349-32928	Sequence 32928, A
c 45	35.6	12.7	3121	7	US-11-293-697-1532	Sequence 1532, Ap
c 46	35.6	12.7	42999	7	US-11-284-877-17	Sequence 17, Appl
47	35.4	12.6	1152	6	US-10-953-349-20671	Sequence 20671, A
c 48	35.4	12.6	1997	7	US-11-293-697-77	Sequence 77, Appl
c 49	35.4	12.6	2628	7	US-11-264-784-50	Sequence 50, Appl
c 50	35.2	12.5	2522	7	US-11-293-697-543	Sequence 543, App

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 04:39:39 ; Search time 6082.82 Seconds  
 (without alignments)  
 2583.230 Million cell updates/sec

Title: US-10-718-955-1  
 Perfect score: 281  
 Sequence: 1 gtgagaaaacactctttcct.....tgccccttaaatcgctccag 281

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

Database : EST:\*  
 1: gb\_est1:\*  
 2: gb\_est3:\*  
 3: gb\_est4:\*  
 4: gb\_est5:\*  
 5: gb\_est6:\*  
 6: gb\_htc:\*  
 7: gb\_est2:\*  
 8: gb\_est7:\*  
 9: gb\_est8:\*  
 10: gb\_est9:\*  
 11: gb\_gss1:\*  
 12: gb\_gss2:\*  
 13: gb\_gss3:\*  
 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
c	1	78.8	28.0	912	5	CK412570			CK412570 AUF_IpGil
c	2	77.6	27.6	692	11	AZ717324			AZ717324 RPCI-24-1
c	3	76.4	27.2	406	14	BX129078			BX129078 Danio rer
c	4	76.4	27.2	452	14	BX173084			BX173084 Danio rer
c	5	76	27.0	278	11	BZ252092			BZ252092 CH230-306
c	6	75.4	26.8	684	14	BX192398			BX192398 Danio rer
c	7	75.2	26.8	191	11	AZ398168			AZ398168 1M0163P19
	8	75.2	26.8	538	14	DU976720			DU976720 AUAC-aaa0

c	9	75	26.7	790	11	BZ141728	BZ141728 CH230-412
c	10	74.8	26.6	639	14	BX129734	BX129734 Danio rer
c	11	74.2	26.4	1014	14	CR133160	CR133160 Forward s
c	12	74	26.3	598	11	BZ143438	BZ143438 CH230-462
c	13	74	26.3	811	14	BX179405	BX179405 Danio rer
c	14	73.8	26.3	610	14	BX198092	BX198092 Danio rer
	15	73.6	26.2	585	14	BX186102	BX186102 Danio rer
c	16	73.6	26.2	757	14	AG607861	AG607861 Mus muscu
c	17	72.8	25.9	596	14	BX176148	BX176148 Danio rer
c	18	72.8	25.9	812	14	BX171590	BX171590 Danio rer
c	19	72.4	25.8	494	4	CB713530	CB713530 AMGNNUC:M
c	20	72.2	25.7	680	14	BX155076	BX155076 Danio rer
c	21	72.2	25.7	816	14	BX221269	BX221269 Danio rer
	22	72	25.6	560	11	AQ981373	AQ981373 RPCI-23-2
c	23	72	25.6	648	11	AZ351589	AZ351589 1M0089P10
c	24	72	25.6	706	11	AZ947453	AZ947453 2M0210J12
c	25	71.8	25.6	613	14	BX157604	BX157604 Danio rer
c	26	71.6	25.5	269	13	CL791416	CL791416 OR_BBa011
	27	71.6	25.5	648	14	BX146163	BX146163 Danio rer
c	28	71.2	25.3	628	7	BF471856	BF471856 UI-M-BH3-
c	29	71.2	25.3	730	14	AG383946	AG383946 Mus muscu
c	30	71.2	25.3	751	14	AG474516	AG474516 Mus muscu
c	31	71.2	25.3	807	11	AQ914771	AQ914771 nbab0049J
c	32	71.2	25.3	1745	2	BM415113	BM415113 OP20184 M
	33	71	25.3	342	14	BX239094	BX239094 Danio rer
c	34	71	25.3	729	14	AG463074	AG463074 Mus muscu
c	35	70.8	25.2	334	14	CR177502	CR177502 Forward s
	36	70.8	25.2	436	14	BX154558	BX154558 Danio rer
c	37	70.8	25.2	533	11	BH105130	BH105130 RPCI-24-4
c	38	70.6	25.1	206	14	DR30113S	AL740566 Danio rer
c	39	70.6	25.1	215	14	DR5L17S	AL733845 Danio rer
c	40	70.6	25.1	605	14	BX218654	BX218654 Danio rer
	41	70.6	25.1	788	14	BX175098	BX175098 Danio rer
c	42	70.2	25.0	789	14	BX159146	BX159146 Danio rer
c	43	70	24.9	350	14	DR25B24T	AL982993 Danio rer
	44	70	24.9	510	14	BX183288	BX183288 Danio rer
	45	70	24.9	592	14	BX180548	BX180548 Danio rer
c	46	70	24.9	715	10	DW283382	DW283382 UI-S-HH0-
c	47	70	24.9	730	14	AG610770	AG610770 Mus muscu
c	48	70	24.9	898	11	BZ122720	BZ122720 CH230-461
	49	69.8	24.8	447	14	BX141934	BX141934 Danio rer
	50	69.8	24.8	572	13	CL989749	CL989749 ZMMBHe000

GenCore version 5.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 04:36:41 ; Search time 195.957 Seconds  
 (without alignments)  
 6853.025 Million cell updates/sec

Title: US-10-718-955-7  
 Perfect score: 21  
 Sequence: 1 cactctttcctatgtatatgc 21

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

Database : GenEmbl:\*  
 1: gb\_env:\*  
 2: gb\_pat:\*  
 3: gb\_ph:\*  
 4: gb\_pl:\*  
 5: gb\_pr:\*  
 6: gb\_ro:\*  
 7: gb\_sts:\*  
 8: gb\_sy:\*  
 9: gb\_un:\*  
 10: gb\_vi:\*  
 11: gb\_ov:\*  
 12: gb\_htg:\*  
 13: gb\_in:\*  
 14: gb\_om:\*  
 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	18.4	87.6	36685	12	AC137637	AC137637 Homo sapi
	2	18.4	87.6	36868	12	AC137493	AC137493 Homo sapi
c	3	18.4	87.6	37480	12	AC137812	AC137812 Homo sapi
	4	18.4	87.6	39732	5	AC137527	AC137527 Homo sapi
	5	18.4	87.6	110000	12	AC139250_0	AC139250 Homo sapi
	6	18.4	87.6	110000	15	AE000657_01	Continuation (2 of
	7	18.4	87.6	148252	12	AC135789	AC135789 Homo sapi

c	8	18.4	87.6	157233	5	AC087564	AC087564 Homo sapi
c	9	18.4	87.6	167662	12	AC135788	AC135788 Homo sapi
c	10	18.4	87.6	210697	12	AC135790	AC135790 Homo sapi
	11	18	85.7	78531	12	AC175508	AC175508 Bos tauru
	12	18	85.7	159934	5	AC097657	AC097657 Homo sapi
	13	18	85.7	167796	12	AC109819	AC109819 Homo sapi
c	14	18	85.7	204190	12	AC140696	AC140696 Rattus no
	15	18	85.7	279534	12	AC114035	AC114035 Rattus no
c	16	17.8	84.8	3253	11	BC094173	BC094173 Xenopus l
c	17	17.8	84.8	110000	4	AP008208_033	Continuation (34 o
c	18	17.8	84.8	110000	12	AC091229_02	Continuation (3 of
	19	17.8	84.8	110000	12	AC091242_0	AC091242 Rattus no
	20	17.8	84.8	110000	12	BX004982_2	Continuation (3 of
	21	17.8	84.8	110000	15	AE016879_32	Continuation (33 o
	22	17.8	84.8	110000	15	AE017225_32	Continuation (33 o
	23	17.8	84.8	110000	15	AE017334_32	Continuation (33 o
c	24	17.8	84.8	111994	11	CR392352	CR392352 Zebrafish
c	25	17.8	84.8	119844	12	AC158446	AC158446 Loxodonta
c	26	17.8	84.8	122070	12	AC175643	AC175643 Loxodonta
c	27	17.8	84.8	123124	12	AC151512	AC151512 Dasypus n
c	28	17.8	84.8	138173	12	AC151513	AC151513 Dasypus n
c	29	17.8	84.8	139177	5	AC097060	AC097060 Homo sapi
c	30	17.8	84.8	141201	12	AC022637	AC022637 Homo sapi
	31	17.8	84.8	141741	5	AC090329	AC090329 Homo sapi
c	32	17.8	84.8	141860	4	AP004126	AP004126 Oryza sat
c	33	17.8	84.8	147178	12	AC026014	AC026014 Homo sapi
	34	17.8	84.8	153099	12	AC149983	AC149983 Strongylo
	35	17.8	84.8	155797	12	AC073049	AC073049 Homo sapi
c	36	17.8	84.8	157466	11	AL928852	AL928852 Zebrafish
	37	17.8	84.8	157606	5	AC090897	AC090897 Homo sapi
c	38	17.8	84.8	162117	6	AC140270	AC140270 Mus muscu
	39	17.8	84.8	162911	5	AC073486	AC073486 Homo sapi
	40	17.8	84.8	164878	12	CT025582	CT025582 Danio rer
	41	17.8	84.8	168473	11	BX649544	BX649544 Zebrafish
c	42	17.8	84.8	169092	12	AC027572	AC027572 Homo sapi
c	43	17.8	84.8	172209	12	CR936422	CR936422 Danio rer
c	44	17.8	84.8	173539	11	CR456632	CR456632 Zebrafish
	45	17.8	84.8	176167	5	AC096656	AC096656 Homo sapi
c	46	17.8	84.8	178875	12	AP001567	AP001567 Homo sapi
c	47	17.8	84.8	180130	12	AC159714	AC159714 Mus muscu
	48	17.8	84.8	181361	12	AC015571	AC015571 Homo sapi
c	49	17.8	84.8	183466	5	AP005241	AP005241 Homo sapi
	50	17.8	84.8	185726	12	AC174686	AC174686 Bos tauru

GenCore version 5.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 04:26:31 ; Search time 70.6718 Seconds  
 (without alignments)  
 2071.790 Million cell updates/sec

Title: US-10-718-955-7  
 Perfect score: 21  
 Sequence: 1 cactctttcctatgtatatgc 21

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

Database : N\_Geneseq\_8:\*  
 1: geneseqn1980s:\*  
 2: geneseqn1990s:\*  
 3: geneseqn2000s:\*  
 4: geneseqn2001as:\*  
 5: geneseqn2001bs:\*  
 6: geneseqn2002as:\*  
 7: geneseqn2002bs:\*  
 8: geneseqn2003as:\*  
 9: geneseqn2003bs:\*  
 10: geneseqn2003cs:\*  
 11: geneseqn2003ds:\*  
 12: geneseqn2004as:\*  
 13: geneseqn2004bs:\*  
 14: geneseqn2005s:\*  
 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	17.8	84.8	110000	12	ADQ97138_1	Continuation (2 of
2	16.8	80.0	9762	4	ABL04410	Abl04410 Drosophil
3	16.8	80.0	35089	14	AED76241	Aed76241 Human CA
4	16.8	80.0	64482	12	ADQ59515	Adq59515 Human can
5	16.8	80.0	64482	14	ADZ13896	Adz13896 Murine ca
6	16.8	80.0	127602	14	AEA61155	Aea61155 Human GLU
7	16.4	78.1	334	9	ACL19379	Ac119379 DNA clone

c	8	16.2	77.1	336	6	ABL84872	Abl84872 Human ova
	9	16.2	77.1	429	4	AAK75496	Aak75496 Human imm
c	10	16.2	77.1	530	5	ABV46429	Abv46429 Human pro
	11	16.2	77.1	551	9	ACH41900	Ach41900 Human foe
	12	16.2	77.1	961	14	AEB67705	Aeb67705 Rice geno
	13	16.2	77.1	1041	5	ABA17818	Aba17818 Human ner
	14	16.2	77.1	1042	5	ABA17819	Aba17819 Human ner
	15	16.2	77.1	1042	5	ABA17820	Aba17820 Human ner
	16	16.2	77.1	1076	6	ABZ70862	Abz70862 Human ATP
c	17	16.2	77.1	1492	3	AAA51403	Aaa51403 Chromosom
c	18	16.2	77.1	1749	6	ABL90045	Abl90045 Human pol
	19	16.2	77.1	1850	3	AAZ33320	Aaz33320 Human sec
	20	16.2	77.1	1902	2	AAV52612	Aav52612 Nucleotid
	21	16.2	77.1	1902	2	AAV52611	Aav52611 Nucleotid
	22	16.2	77.1	2332	10	ADA53832	Ada53832 Human cod
	23	16.2	77.1	2780	4	AAK94287	Aak94287 Human ful
	24	16.2	77.1	2780	12	ADL30899	Adl30899 Full leng
	25	16.2	77.1	2925	3	AAA75156	Aaa75156 cDNA enco
	26	16.2	77.1	3025	10	ADC42880	Adc42880 REMAP enc
c	27	16.2	77.1	3046	4	AAH54418	Aah54418 S. epider
	28	16.2	77.1	3751	11	AEA90321	Aea90321 Human NOV
	29	16.2	77.1	14789	4	ABL29350	Abl29350 Drosophil
	30	16.2	77.1	40085	14	AEA61140	Aea61140 Human FMO
	31	16.2	77.1	103738	14	ADX06943	Adx06943 Cyclin-de
c	32	16.2	77.1	110000	5	AAI61373_0	Aai61373 Soybean 3
	33	16.2	77.1	171398	14	ADZ13359	Adz13359 Human can
	34	16.2	77.1	191584	13	ABD33586	Abd33586 Human can
	35	16.2	77.1	191584	13	ADR67026	Adr67026 Human can
c	36	16.2	77.1	194266	14	AED76144	Aed76144 Mouse CA
	37	16	76.2	402	13	ACF90718	Acf90718 Human SIR
c	38	16	76.2	1933	14	AEB35306	Aeb35306 Human Gef
c	39	16	76.2	2907	10	ACC72694	Acc72694 Human can
c	40	15.8	75.2	52	8	ACC79604	Acc79604 Skp gene
c	41	15.8	75.2	52	10	ADE29212	Ade29212 Multivale
c	42	15.8	75.2	52	12	ADM32738	Adm32738 PCR prime
	43	15.8	75.2	185	9	ACL19389	Ac119389 DNA clone
	44	15.8	75.2	286	10	ABX82684	Abx82684 Corn ear-
	45	15.8	75.2	342	9	ACL19391	Ac119391 DNA clone
	46	15.8	75.2	357	9	ACL19394	Ac119394 DNA clone
c	47	15.8	75.2	373	2	AAQ43724	Aaq43724 Sequence
c	48	15.8	75.2	373	2	AAX16669	Aax16669 Bovine Y
	49	15.8	75.2	531	9	ACL19386	Ac119386 DNA clone
	50	15.8	75.2	548	9	ACL19385	Ac119385 DNA clone
	51	15.8	75.2	549	9	ACL19381	Ac119381 DNA clone
	52	15.8	75.2	567	9	ACL19392	Ac119392 DNA clone
	53	15.8	75.2	573	9	ACL19383	Ac119383 DNA clone
c	54	15.8	75.2	577	10	AAD50050	Aad50050 Human fat
	55	15.8	75.2	592	9	ACL19393	Ac119393 DNA clone
	56	15.8	75.2	598	9	ACL19388	Ac119388 DNA clone
	57	15.8	75.2	601	9	ACL19382	Ac119382 DNA clone
	58	15.8	75.2	604	9	ACL19390	Ac119390 DNA clone
	59	15.8	75.2	604	9	ACL19384	Ac119384 DNA clone

GenCore version 5.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 04:56:26 ; Search time 20.0898 Seconds  
 (without alignments)  
 1955.884 Million cell updates/sec

Title: US-10-718-955-7  
 Perfect score: 21  
 Sequence: 1 cactcttttcctatgtatatgc 21

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

Database : Issued\_Patents\_NA:\*  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*  
 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
c 1	17.4	82.9		601	3	US-09-949-016-73589	Sequence 73589, A
c 2	17.4	82.9		601	3	US-09-949-016-73590	Sequence 73590, A
c 3	17.4	82.9		601	3	US-09-949-016-73591	Sequence 73591, A
c 4	17.4	82.9		601	3	US-09-949-016-73608	Sequence 73608, A
c 5	17.4	82.9		601	3	US-09-949-016-73609	Sequence 73609, A
c 6	17.4	82.9		601	3	US-09-949-016-73610	Sequence 73610, A
7	17.4	82.9	38705	3	3	US-09-949-016-13883	Sequence 13883, A
8	17.4	82.9	38705	3	3	US-09-949-016-13884	Sequence 13884, A
9	16.2	77.1	601	3	3	US-09-949-016-78652	Sequence 78652, A
c 10	16.2	77.1	601	3	3	US-09-949-016-177508	Sequence 177508, A
11	16.2	77.1	1902	3	3	US-09-041-991A-7	Sequence 7, Appli
12	16.2	77.1	1902	3	3	US-09-041-991A-9	Sequence 9, Appli

	13	16.2	77.1	1902	3	US-09-608-533A-7	Sequence 7, Appli
	14	16.2	77.1	1902	3	US-09-608-533A-9	Sequence 9, Appli
	15	16.2	77.1	2332	4	US-10-094-749-1400	Sequence 1400, Ap
c	16	16.2	77.1	3046	3	US-09-710-279-3782	Sequence 3782, Ap
	17	16.2	77.1	43086	3	US-09-949-016-13059	Sequence 13059, A
c	18	16.2	77.1	65300	3	US-09-949-016-16813	Sequence 16813, A
	19	16.2	77.1	91831	3	US-09-949-016-13694	Sequence 13694, A
	20	16.2	77.1	107421	3	US-09-949-016-15532	Sequence 15532, A
	21	16.2	77.1	135667	3	US-09-949-016-15051	Sequence 15051, A
c	22	16.2	77.1	168971	3	US-09-949-016-13807	Sequence 13807, A
	23	16.2	77.1	784019	3	US-09-949-016-14033	Sequence 14033, A
	24	16.2	77.1	828152	3	US-09-949-016-12777	Sequence 12777, A
	25	15.8	75.2	92	2	US-07-839-751-1	Sequence 1, Appli
	26	15.8	75.2	92	2	US-08-239-427A-1	Sequence 1, Appli
	27	15.8	75.2	92	2	US-08-467-975-1	Sequence 1, Appli
	28	15.8	75.2	92	3	US-08-401-355-1	Sequence 1, Appli
	29	15.8	75.2	92	5	US-09-389-364-1	Sequence 1, Appli
	30	15.8	75.2	286	3	US-09-313-294A-1144	Sequence 1144, Ap
c	31	15.8	75.2	373	2	US-07-984-044A-6	Sequence 6, Appli
c	32	15.8	75.2	373	2	US-08-458-393-6	Sequence 6, Appli
c	33	15.8	75.2	601	3	US-09-949-016-22618	Sequence 22618, A
	34	15.8	75.2	601	3	US-09-949-016-142485	Sequence 142485,
c	35	15.8	75.2	601	3	US-09-949-016-164863	Sequence 164863,
c	36	15.8	75.2	601	3	US-09-949-016-171682	Sequence 171682,
c	37	15.8	75.2	1508	3	US-09-270-767-13043	Sequence 13043, A
	38	15.8	75.2	3383	3	US-08-884-324-12	Sequence 12, Appl
	39	15.8	75.2	3383	3	US-09-479-862-12	Sequence 12, Appl
c	40	15.8	75.2	3808	2	US-08-417-210A-79	Sequence 79, Appl
c	41	15.8	75.2	3808	3	US-09-136-159A-79	Sequence 79, Appl
c	42	15.8	75.2	3879	3	US-09-638-715-35	Sequence 35, Appl
c	43	15.8	75.2	3879	3	US-10-060-509-35	Sequence 35, Appl
c	44	15.8	75.2	3879	3	US-10-060-506-35	Sequence 35, Appl
c	45	15.8	75.2	7616	3	US-08-815-809-6	Sequence 6, Appli
c	46	15.8	75.2	7797	2	US-08-816-155B-7	Sequence 7, Appli
c	47	15.8	75.2	7797	3	US-09-079-587-7	Sequence 7, Appli
c	48	15.8	75.2	10962	2	US-08-816-155B-6	Sequence 6, Appli
c	49	15.8	75.2	10962	3	US-09-079-587-6	Sequence 6, Appli
	50	15.8	75.2	11464	3	US-08-884-324-13	Sequence 13, Appl
	51	15.8	75.2	11464	3	US-09-479-862-13	Sequence 13

GenCore version 5.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 05:16:51 ; Search time 132.762 Seconds  
 (without alignments)  
 1943.637 Million cell updates/sec

Title: US-10-718-955-7  
 Perfect score: 21  
 Sequence: 1 cactcttttcctatgtatatgc 21

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

Database : Published\_Applications\_NA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
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- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	17.8	84.8	595	4	US-09-925-065A-107539	Sequence 107539,
c	2	17.8	84.8	595	5	US-09-925-065A-107539	Sequence 107539,
c	3	17.8	84.8	596	6	US-10-027-632-210863	Sequence 210863,
c	4	17.8	84.8	596	7	US-10-027-632-210863	Sequence 210863,
c	5	17.8	84.8	596	12	US-10-301-480-207393	Sequence 207393,
c	6	17.8	84.8	596	12	US-10-301-480-820802	Sequence 820802,

	7	17.8	84.8	440684	11	US-10-330-773-114	Sequence 114, App
c	8	17.4	82.9	586	4	US-09-925-065A-640877	Sequence 640877,
c	9	17.4	82.9	586	5	US-09-925-065A-640877	Sequence 640877,
c	10	17.4	82.9	640	6	US-10-027-632-291073	Sequence 291073,
c	11	17.4	82.9	640	7	US-10-027-632-291073	Sequence 291073,
c	12	17.4	82.9	680	6	US-10-027-632-133109	Sequence 133109,
c	13	17.4	82.9	680	6	US-10-027-632-133110	Sequence 133110,
c	14	17.4	82.9	680	6	US-10-027-632-133111	Sequence 133111,
c	15	17.4	82.9	680	7	US-10-027-632-133109	Sequence 133109,
c	16	17.4	82.9	680	7	US-10-027-632-133110	Sequence 133110,
c	17	17.4	82.9	680	7	US-10-027-632-133111	Sequence 133111,
c	18	17.4	82.9	2105	6	US-10-027-632-103335	Sequence 103335,
c	19	17.4	82.9	2105	7	US-10-027-632-103335	Sequence 103335,
c	20	17	81.0	632	4	US-09-925-065A-678836	Sequence 678836,
c	21	17	81.0	632	5	US-09-925-065A-678836	Sequence 678836,
c	22	16.8	80.0	201	9	US-10-719-993-8266	Sequence 8266, Ap
	23	16.8	80.0	367	4	US-09-925-065A-584795	Sequence 584795,
	24	16.8	80.0	367	4	US-09-925-065A-584796	Sequence 584796,
	25	16.8	80.0	367	5	US-09-925-065A-584795	Sequence 584795,
	26	16.8	80.0	367	5	US-09-925-065A-584796	Sequence 584796,
c	27	16.8	80.0	406	10	US-10-972-079-44040	Sequence 44040, A
	28	16.8	80.0	415	8	US-10-424-599-103954	Sequence 103954,
c	29	16.8	80.0	456	10	US-10-972-079-44039	Sequence 44039, A
c	30	16.8	80.0	535	4	US-09-925-065A-489537	Sequence 489537,
c	31	16.8	80.0	535	5	US-09-925-065A-489537	Sequence 489537,
	32	16.8	80.0	620	12	US-10-301-480-38204	Sequence 38204, A
	33	16.8	80.0	620	12	US-10-301-480-651613	Sequence 651613,
	34	16.8	80.0	628	12	US-10-301-480-297361	Sequence 297361,
	35	16.8	80.0	628	12	US-10-301-480-297362	Sequence 297362,
	36	16.8	80.0	628	12	US-10-301-480-297363	Sequence 297363,
	37	16.8	80.0	628	12	US-10-301-480-910770	Sequence 910770,
	38	16.8	80.0	628	12	US-10-301-480-910771	Sequence 910771,
	39	16.8	80.0	628	12	US-10-301-480-910772	Sequence 910772,
	40	16.8	80.0	633	4	US-09-925-065A-757438	Sequence 757438,
	41	16.8	80.0	633	5	US-09-925-065A-757438	Sequence 757438,
	42	16.8	80.0	634	4	US-09-925-065A-209971	Sequence 209971,
	43	16.8	80.0	634	4	US-09-925-065A-209972	Sequence 209972,
	44	16.8	80.0	634	4	US-09-925-065A-209973	Sequence 209973,
	45	16.8	80.0	634	5	US-09-925-065A-209971	Sequence 209971,
	46	16.8	80.0	634	5	US-09-925-065A-209972	Sequence 209972,
	47	16.8	80.0	634	5	US-09-925-065A-209973	Sequence 209973,
	48	16.8	80.0	679	12	US-10-301-480-608445	Sequence 608445,
	49	16.8	80.0	679	12	US-10-301-480-1221854	Sequence 1221854,
c	50	16.8	80.0	735	4	US-09-925-065A-27939	Sequence 27939, A

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 05:18:23 ; Search time 4.03096 Seconds  
 (without alignments)  
 588.091 Million cell updates/sec

Title: US-10-718-955-7  
 Perfect score: 21  
 Sequence: 1 cactctttcctatgtatatgc 21

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

Database : Published\_Applications\_NA\_New:\*  
 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
	1	15.8	75.2	3235	6	US-10-953-349-1287
c	2	15.4	73.3	348	7	US-11-217-529-76030
	3	15.4	73.3	1821	7	US-11-217-529-78440
c	4	15.2	72.4	588	6	US-10-488-619-2328
	5	15.2	72.4	833	6	US-10-488-619-2327
	6	15.2	72.4	1191	6	US-10-953-349-19282
c	7	15.2	72.4	1449	6	US-10-953-349-19091
c	8	15.2	72.4	1471	6	US-10-953-349-18869
c	9	15.2	72.4	1798	6	US-10-953-349-5065
	10	15.2	72.4	70665	6	US-10-505-928-596
c	11	14.8	70.5	51	7	US-11-143-642-727
c	12	14.8	70.5	2126	7	US-11-293-697-1258
	13	14.8	70.5	2376	7	US-11-293-697-2332
	14	14.8	70.5	2755	7	US-11-293-697-211

c	15	14.8	70.5	2857	6	US-10-196-749-105	Sequence 105, App
	16	14.8	70.5	3112	7	US-11-293-697-887	Sequence 887, App
	17	14.8	70.5	3428	6	US-10-511-455-51	Sequence 51, Appl
	18	14.8	70.5	3547	7	US-11-293-697-832	Sequence 832, App
	19	14.6	69.5	876	6	US-10-488-619-2828	Sequence 2828, Ap
	20	14.6	69.5	2572	6	US-10-953-349-2910	Sequence 2910, Ap
	21	14.6	69.5	6826	6	US-10-505-928-330	Sequence 330, App
	22	14.6	69.5	128361	6	US-10-505-928-151	Sequence 151, App
c	23	14.4	68.6	518	7	US-11-301-554-769	Sequence 769, App
	24	14.4	68.6	909	7	US-11-217-529-82140	Sequence 82140, A
c	25	14.4	68.6	2259	6	US-10-953-349-22975	Sequence 22975, A
	26	14.4	68.6	2646	7	US-11-293-697-668	Sequence 668, App
c	27	14.4	68.6	394191	6	US-10-506-549-3	Sequence 3, Appli
	28	14.2	67.6	72	7	US-11-194-055-226	Sequence 226, App
	29	14.2	67.6	72	7	US-11-194-055-281	Sequence 281, App
c	30	14.2	67.6	534	7	US-11-217-529-76	Sequence 76, Appl
	31	14.2	67.6	553	6	US-10-488-619-1138	Sequence 1138, Ap
c	32	14.2	67.6	577	6	US-10-488-619-1139	Sequence 1139, Ap
	33	14.2	67.6	903	7	US-11-217-529-3323	Sequence 3323, Ap
c	34	14.2	67.6	1383	6	US-10-953-349-11043	Sequence 11043, A
	35	14.2	67.6	1431	7	US-11-217-529-3429	Sequence 3429, Ap
	36	14.2	67.6	1437	7	US-11-217-529-78974	Sequence 78974, A
	37	14.2	67.6	1776	6	US-10-953-349-2115	Sequence 2115, Ap
c	38	14.2	67.6	1866	7	US-11-217-529-148	Sequence 148, App
c	39	14.2	67.6	2007	7	US-11-293-697-1897	Sequence 1897, Ap
c	40	14.2	67.6	2589	7	US-11-217-529-78347	Sequence 78347, A
	41	14.2	67.6	3381	7	US-11-293-697-1123	Sequence 1123, Ap
c	42	14.2	67.6	4197	7	US-11-217-529-79360	Sequence 79360, A
c	43	14.2	67.6	4611	7	US-11-217-529-2741	Sequence 2741, Ap
	44	14.2	67.6	4852	6	US-10-505-928-417	Sequence 417, App
c	45	14.2	67.6	9801	7	US-11-217-529-636	Sequence 636, App
	46	14	66.7	1470	7	US-11-217-529-76116	Sequence 76116, A
	47	13.8	65.7	25	7	US-11-217-529-56920	Sequence 56920, A
c	48	13.8	65.7	354	7	US-11-301-554-1788	Sequence 1788, Ap
c	49	13.8	65.7	744	6	US-10-953-349-39912	Sequence 39912, A
	50	13.8	65.7	917	6	US-10-953-349-17483	Sequence 17483, A
	51	13.8	65.7	924	7	US-11-217-529-4585	Sequence 4585, Ap
	52	13.8	65.7	1121	6	US-10-953-349-6533	Sequence 6533, Ap
	53	13.8	65.7	1134	7	US-11-217-529-75591	Sequence 75591, A
c	54	13.8	65.7	1155	6	US-10-953-349-6668	Sequence 6668, Ap
c	55	13.8	65.7	1224	7	US-11-217-529-78266	Sequence 78266, A
c	56	13.8	65.7	1287	7	US-11-217-529-2869	Sequence 2869, Ap
c	57	13.8	65.7	1296	7	US-11-217-529-173598	Sequence 173598,
	58	13.8	65.7	1678	6	US-10-953-349-11625	Sequence

GenCore version 5.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 04:39:39 ; Search time 454.588 Seconds  
 (without alignments)  
 2583.230 Million cell updates/sec

Title: US-10-718-955-7  
 Perfect score: 21  
 Sequence: 1 cactcttttcctatgtatatgc 21

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

Database : EST:\*  
 1: gb\_est1:\*  
 2: gb\_est3:\*  
 3: gb\_est4:\*  
 4: gb\_est5:\*  
 5: gb\_est6:\*  
 6: gb\_htc:\*  
 7: gb\_est2:\*  
 8: gb\_est7:\*  
 9: gb\_est8:\*  
 10: gb\_est9:\*  
 11: gb\_gss1:\*  
 12: gb\_gss2:\*  
 13: gb\_gss3:\*  
 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	21	100.0	684	12	CE798192	CE798192 tigr-gss-
	2	21	100.0	724	12	CE773639	CE773639 tigr-gss-
	3	18.4	87.6	500	12	CE708194	CE708194 tigr-gss-
	4	18.4	87.6	631	2	BJ824737	BJ824737 BJ824737
c	5	18.4	87.6	671	14	AG178927	AG178927 Pan trogl
c	6	18	85.7	517	13	CL355721	CL355721 RPCI44_41
	7	18	85.7	620	11	BZ179705	BZ179705 CH230-484
c	8	17.8	84.8	225	11	BH228958	BH228958 1006149D1

	9	17.8	84.8	266	2	BM130076	BM130076 pb26b10.y
c	10	17.8	84.8	356	4	CB813776	CB813776 AMGNNUC:S
c	11	17.8	84.8	362	11	BH228959	BH228959 1006149D1
c	12	17.8	84.8	418	4	CB765602	CB765602 AMGNNUC:S
c	13	17.8	84.8	464	12	CE758709	CE758709 tigr-gss-
c	14	17.8	84.8	475	12	CC772331	CC772331 CH240_8I8
	15	17.8	84.8	527	9	DN797464	DN797464 USDA-FP/A
c	16	17.8	84.8	540	11	B54581	B54581 CIT-HSP-347
	17	17.8	84.8	575	11	BH274944	BH274944 CH230-1B1
c	18	17.8	84.8	758	10	DV370743	DV370743 NACMV07TO
	19	17.8	84.8	835	11	BZ142352	BZ142352 CH230-245
	20	17.8	84.8	898	5	CK418265	CK418265 AUF_IpInt
c	21	17.8	84.8	1457	14	AG463632	AG463632 Mus muscu
c	22	17.4	82.9	359	11	AQ031752	AQ031752 HS_2225_B
	23	17.4	82.9	399	12	CE569004	CE569004 tigr-gss-
c	24	17.4	82.9	416	1	AA724080	AA724080 ah98g09.s
c	25	17.4	82.9	422	11	AQ030469	AQ030469 HS_2183_A
	26	17.4	82.9	456	11	BH338663	BH338663 CH230-194
	27	17.4	82.9	466	13	CL875526	CL875526 abf04c07.
c	28	17.4	82.9	514	7	AW274464	AW274464 xv30a04.x
	29	17.4	82.9	520	14	DX234758	DX234758 OR_ABa011
	30	17.4	82.9	536	11	BH264523	BH264523 CH230-91C
c	31	17.4	82.9	562	11	AQ987060	AQ987060 RPCI-23-3
c	32	17.4	82.9	606	12	CE473448	CE473448 tigr-gss-
c	33	17.4	82.9	714	14	AG090255	AG090255 Pan trogl
	34	17.4	82.9	780	14	DX189320	DX189320 OR_ABa005
c	35	17.4	82.9	826	14	CT247514	CT247514 Sus scrof
c	36	17.4	82.9	861	1	AL562437	AL562437 AL562437
c	37	17.4	82.9	1138	12	CL147276	CL147276 ISB1-156L
	38	17.4	82.9	1222	9	DN479787	DN479787 altr016xl
	39	17.4	82.9	1514	6	CR594909	CR594909 full-leng
	40	17	81.0	524	14	AG249431	AG249431 Lotus cor
c	41	17	81.0	527	14	AG228939	AG228939 Lotus cor
c	42	17	81.0	551	3	BU994853	BU994853 HM08G14r
	43	17	81.0	641	14	CR149250	CR149250 Reverse s
	44	17	81.0	677	12	CC769666	CC769666 CH240_134
	45	17	81.0	688	1	AJ502427	AJ502427 AJ502427
	46	17	81.0	711	3	BU460510	BU460510 603777237
c	47	17	81.0	751	10	DR916445	DR916445 EST110798
	48	17	81.0	843	14	CT283381	CT283381 Sus scrof
c	49	17	81.0	861	10	DT740848	DT740848 EST117469
	50	17	81.0	887	14	CT398723	CT398723 Sus scrof
	51	17	81.0	902	10	DR931356	DR931356 EST112289
c	52	17	81.0	934	14	CNS00C40	AL058421 Drosophil
c	53	17	81.0	957	10	DR931355	DR931355 EST112289

GenCore version 5.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 04:36:41 ; Search time 195.957 Seconds  
 (without alignments)  
 6853.025 Million cell updates/sec

Title: US-10-718-955-8  
 Perfect score: 21  
 Sequence: 1 cgattttaaggggcaagtttagc 21

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

Database : GenEmbl:\*  
 1: gb\_env:\*  
 2: gb\_pat:\*  
 3: gb\_ph:\*  
 4: gb\_pl:\*  
 5: gb\_pr:\*  
 6: gb\_ro:\*  
 7: gb\_sts:\*  
 8: gb\_sy:\*  
 9: gb\_un:\*  
 10: gb\_vi:\*  
 11: gb\_ov:\*  
 12: gb\_htg:\*  
 13: gb\_in:\*  
 14: gb\_om:\*  
 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	17.8	84.8	65013	12	AC163822	AC163822 Bos tauru
c	2	17.4	82.9	153019	6	AC120156	AC120156 Mus muscu
c	3	17.4	82.9	165328	5	AC022929	AC022929 Homo sapi
	4	17.4	82.9	174690	12	AC163941	AC163941 Bos tauru
c	5	17.4	82.9	203641	6	AL845297	AL845297 Mouse DNA
	6	17.4	82.9	214941	12	AC150409	AC150409 Branchios
c	7	17	81.0	154025	12	AC142058	AC142058 Rattus no

	8	17	81.0	177071	12	AC128090	AC128090 Rattus no
c	9	17	81.0	214241	12	AC157426	AC157426 Bos tauru
c	10	17	81.0	229506	12	AC160328	AC160328 Bos tauru
c	11	17	81.0	252738	12	AC159838	AC159838 Bos tauru
	12	16.8	80.0	344	4	AF035390	AF035390 Armillari
	13	16.8	80.0	101682	12	AC091468	AC091468 Mus muscu
c	14	16.8	80.0	130665	6	AF289666	AF289666 Mus muscu
	15	16.8	80.0	138507	6	AC120390	AC120390 Mus muscu
	16	16.8	80.0	150795	12	AC168182	AC168182 Muntiacus
	17	16.8	80.0	150851	11	BX927068	BX927068 Zebrafish
c	18	16.8	80.0	154561	5	AC021355	AC021355 Homo sapi
c	19	16.8	80.0	167128	12	AC164503	AC164503 Sus scrof
	20	16.8	80.0	168308	12	AC169459	AC169459 Muntiacus
	21	16.8	80.0	170072	6	AC116329	AC116329 Mus muscu
	22	16.8	80.0	177225	4	BX908808	BX908808 Neurospor
	23	16.8	80.0	179404	12	AC175756	AC175756 Bos tauru
c	24	16.8	80.0	179790	6	AC167419	AC167419 Mus muscu
	25	16.8	80.0	182945	12	AC141518	AC141518 Rattus no
	26	16.8	80.0	183318	6	AL844856	AL844856 Mouse DNA
c	27	16.8	80.0	185786	12	AC079372	AC079372 Mus muscu
	28	16.8	80.0	191322	6	AC140314	AC140314 Mus muscu
	29	16.8	80.0	195225	12	AC023930	AC023930 Homo sapi
	30	16.8	80.0	197774	12	CR626902	CR626902 Danio rer
	31	16.8	80.0	201747	12	AC163876	AC163876 Bos tauru
	32	16.8	80.0	205602	6	AF325177	AF325177 Mus muscu
c	33	16.8	80.0	217804	12	AC117297	AC117297 Rattus no
	34	16.8	80.0	223529	6	AC137871	AC137871 Mus muscu
	35	16.8	80.0	224961	12	AC107529	AC107529 Rattus no
c	36	16.8	80.0	235976	12	AC119627	AC119627 Rattus no
	37	16.8	80.0	245942	12	AC121374	AC121374 Rattus no
	38	16.8	80.0	246613	12	AC161077	AC161077 Bos tauru
c	39	16.8	80.0	248528	12	AC095666	AC095666 Rattus no
	40	16.8	80.0	250578	12	AC173126	AC173126 Bos tauru
	41	16.8	80.0	254581	12	AC097817	AC097817 Rattus no
c	42	16.8	80.0	268268	12	AC129154	AC129154 Rattus

# SCORE Search Results Details for Application 10 10-718-955-8.200hits.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10718955 and Search Result us-10-7:  
[start](#) | [next page](#)

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 04:36:41 ; Search time 195.957 Seconds  
(without alignments)  
6853.025 Million cell updates/sec

Title: US-10-718-955-8  
Perfect score: 21  
Sequence: 1 cgatttaaggggcaagtttagc 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 600 summaries

Database : GenEmbl:\*  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_htg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
c 1	17.8	84.8	65013	12	AC163822	AC163822 Bos tauru
c 2	17.4	82.9	153019	6	AC120156	AC120156 Mus muscu
c 3	17.4	82.9	165328	5	AC022929	AC022929 Homo sapi
c 4	17.4	82.9	174690	12	AC163941	AC163941 Bos tauru
c 5	17.4	82.9	203641	6	AL845297	AL845297 Mouse DNA
c 6	17.4	82.9	214941	12	AC150409	AC150409 Branchios
c 7	17	81.0	154025	12	AC142058	AC142058 Rattus no
c 8	17	81.0	177071	12	AC128090	AC128090 Rattus no
c 9	17	81.0	214241	12	AC157426	AC157426 Bos tauru
c 10	17	81.0	229506	12	AC160328	AC160328 Bos tauru
c 11	17	81.0	252738	12	AC159838	AC159838 Bos tauru
c 12	16.8	80.0	344	4	AF035390	AF035390 Armillari
c 13	16.8	80.0	101682	12	AC091468	AC091468 Mus muscu
c 14	16.8	80.0	130665	6	AF289666	AF289666 Mus muscu
c 15	16.8	80.0	138507	6	AC120390	AC120390 Mus muscu
c 16	16.8	80.0	150795	12	AC168182	AC168182 Muntiacus
c 17	16.8	80.0	150851	11	BX927068	BX927068 Zebrafish
c 18	16.8	80.0	154561	5	AC021355	AC021355 Homo sapi
c 19	16.8	80.0	167128	12	AC164503	AC164503 Sus scrof
c 20	16.8	80.0	168308	12	AC169459	AC169459 Muntiacus
c 21	16.8	80.0	170072	6	AC116329	AC116329 Mus muscu
c 22	16.8	80.0	177225	4	BX908808	BX908808 Neurospor
c 23	16.8	80.0	179404	12	AC175756	AC175756 Bos tauru
c 24	16.8	80.0	179790	6	AC167419	AC167419 Mus muscu
c 25	16.8	80.0	182945	12	AC141518	AC141518 Rattus no
c 26	16.8	80.0	183318	6	AL844856	AL844856 Mouse DNA
c 27	16.8	80.0	185786	12	AC079372	AC079372 Mus muscu
c 28	16.8	80.0	191322	6	AC140314	AC140314 Mus muscu
c 29	16.8	80.0	195225	12	AC023930	AC023930 Homo sapi
c 30	16.8	80.0	197774	12	CR626902	CR626902 Danio rer
c 31	16.8	80.0	201747	12	AC163876	AC163876 Bos tauru
c 32	16.8	80.0	205602	6	AF325177	AF325177 Mus muscu
c 33	16.8	80.0	217804	12	AC117297	AC117297 Rattus no
c 34	16.8	80.0	223529	6	AC137871	AC137871 Mus muscu
c 35	16.8	80.0	224961	12	AC107529	AC107529 Rattus no
c 36	16.8	80.0	235976	12	AC119627	AC119627 Rattus no
c 37	16.8	80.0	245942	12	AC121374	AC121374 Rattus no
c 38	16.8	80.0	246613	12	AC161077	AC161077 Bos tauru
c 39	16.8	80.0	248528	12	AC095666	AC095666 Rattus no
c 40	16.8	80.0	250578	12	AC173126	AC173126 Bos tauru
c 41	16.8	80.0	254581	12	AC097817	AC097817 Rattus no
c 42	16.8	80.0	268268	12	AC129154	AC129154 Rattus no
c 43	16.8	80.0	271233	12	AC096597	AC096597 Rattus no
c 44	16.8	80.0	272578	12	AC108338	AC108338 Rattus no
c 45	16.8	80.0	275588	12	AC170383	AC170383 Bos tauru
c 46	16.4	78.1	777	2	CQ414343	CQ414343 Sequence
c 47	16.4	78.1	33481	2	CQ576842	CQ576842 Sequence
c 48	16.4	78.1	37727	12	AC014119	AC014119 Drosophil
c 49	16.4	78.1	65548	12	AC118270	AC118270 Homo sapi
c 50	16.4	78.1	66374	12	AC013501	AC013501 Homo sapi
c 51	16.4	78.1	67648	12	AC010817	AC010817 Homo sapi
c 52	16.4	78.1	76587	5	AL390954	AL390954 Human DNA
c 53	16.4	78.1	77908	5	AC008609	AC008609 Homo sapi
c 54	16.4	78.1	95484	12	AC015854	AC015854 Homo sapi
c 55	16.4	78.1	100240	6	AL713968	AL713968 Mouse DNA
c 56	16.4	78.1	102564	5	AC015916	AC015916 Homo sapi

GenCore version 5.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 04:56:26 ; Search time 20.0898 Seconds  
 (without alignments)  
 1955.884 Million cell updates/sec

Title: US-10-718-955-8  
 Perfect score: 21  
 Sequence: 1 cgattttaaggggcaagtttagc 21

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

Database : Issued\_Patents\_NA:\*  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*  
 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	15.8	75.2	2306	2	US-08-378-698-3	Sequence 3, Appli
2	15.8	75.2	2306	7	PCT-US96-00728-3	Sequence 3, Appli
3	15.8	75.2	34185	3	US-09-545-481-3	Sequence 3, Appli
c 4	15.8	75.2	90776	3	US-09-949-016-17230	Sequence 17230, A
c 5	15.8	75.2	162465	3	US-09-949-016-14264	Sequence 14264, A
c 6	15.4	73.3	390	3	US-09-107-532A-660	Sequence 660, App
7	15.4	73.3	601	3	US-09-949-016-192231	Sequence 192231,
8	15.4	73.3	672	5	US-09-974-300-5192	Sequence 5192, Ap
9	15.4	73.3	921	5	US-09-974-300-5200	Sequence 5200, Ap
10	15.4	73.3	42595	5	US-09-984-429-469	Sequence 469, App
c 11	15.2	72.4	511	3	US-09-902-540-1611	Sequence 1611, Ap
12	15.2	72.4	601	3	US-09-949-016-65226	Sequence 65226, A

	13	15.2	72.4	601	3	US-09-949-016-80017	Sequence 80017, A
c	14	15.2	72.4	601	3	US-09-949-016-162733	Sequence 162733,
c	15	15.2	72.4	601	3	US-09-949-016-181489	Sequence 181489,
c	16	15.2	72.4	601	3	US-09-949-016-181490	Sequence 181490,
c	17	15.2	72.4	601	3	US-09-949-016-181491	Sequence 181491,
c	18	15.2	72.4	601	3	US-09-949-016-181492	Sequence 181492,
c	19	15.2	72.4	1746	3	US-09-583-110-350	Sequence 350, App
c	20	15.2	72.4	1788	3	US-09-107-433-29	Sequence 29, Appl
	21	15.2	72.4	2274	3	US-09-494-297A-1	Sequence 1, Appli
c	22	15.2	72.4	2439	3	US-09-949-016-1904	Sequence 1904, Ap
c	23	15.2	72.4	2475	4	US-09-874-198-3	Sequence 3, Appli
	24	15.2	72.4	3366	3	US-09-775-398-86	Sequence 86, Appl
	25	15.2	72.4	6596	3	US-09-575-602-11	Sequence 11, Appl
	26	15.2	72.4	6596	3	US-09-032-086-11	Sequence 11, Appl
c	27	15.2	72.4	13188	3	US-08-961-527-70	Sequence 70, Appl
c	28	15.2	72.4	23640	3	US-09-949-016-13646	Sequence 13646, A
c	29	15.2	72.4	25220	5	US-09-984-429-364	Sequence 364, App
	30	15.2	72.4	30221	3	US-09-949-016-12577	Sequence 12577, A
	31	15.2	72.4	30222	3	US-09-949-016-17299	Sequence 17299, A
	32	15.2	72.4	78649	3	US-09-949-016-14619	Sequence 14619, A
	33	15.2	72.4	78649	3	US-09-949-016-14620	Sequence 14620, A
	34	15.2	72.4	78649	3	US-09-949-016-16227	Sequence 16227, A
	35	15.2	72.4	78649	3	US-09-949-016-16228	Sequence 16228, A
c	36	15.2	72.4	125672	3	US-09-949-016-16956	Sequence 16956, A
c	37	15.2	72.4	140925	3	US-09-949-016-11777	Sequence 11777, A
c	38	15.2	72.4	140982	3	US-09-949-016-16295	Sequence 16295, A
c	39	15.2	72.4	236341	3	US-09-949-016-13978	Sequence 13978, A
c	40	15.2	72.4	271134	3	US-09-949-016-12705	Sequence 12705, A
c	41	15.2	72.4	305491	3	US-09-949-016-17550	Sequence 17550, A
	42	15.2	72.4	312470	3	US-09-949-016-14043	Sequence 14043, A
	43	15.2	72.4	336024	3	US-09-949-016-12373	Sequence 12373, A
c	44	15	71.4	601	3	US-09-949-016-19643	Sequence 19643, A
c	45	15	71.4	601	3	US-09-949-016-19644	Sequence 19644, A
	46	15	71.4	601	3	US-09-949-016-72689	Sequence 72689, A
	47	15	71.4	601	3	US-09-949-016-72690	Sequence 72690, A
c	48	15	71.4	601	3	US-09-949-016-118103	Sequence 118103,
c	49	15	71.4	601	3	US-09-949-016-118104	Sequence 118104,
c	50	15	71.4	55264	3	US-09-949-016-15014	Sequence 15014, A
c	51	15	71.4	94755	3	US-09-949-016-11839	Sequence 11839, A
c	52	15	71.4	137394	3	US-09-949-016-13872	Sequence 13872, A
c	53	15	71.4	137743	3	US-09-949-016-12178	Sequence 12178, A
c	54	15	71.4	385136	3	US-09-949-016-16073	Sequence 16073

GenCore version 5.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 05:18:23 ; Search time 4.03096 Seconds  
 (without alignments)  
 588.091 Million cell updates/sec

Title: US-10-718-955-8  
 Perfect score: 21  
 Sequence: 1 cgatttaaggggcaagtttagc 21

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

Database : Published\_Applications\_NA\_New:\*  
 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
1	14.8	70.5	822	7	US-11-217-529-191079	Sequence 191079,
2	14.8	70.5	1416	7	US-11-217-529-576	Sequence 576, App
c 3	14.6	69.5	702	7	US-11-217-529-1047	Sequence 1047, Ap
4	14.6	69.5	747	7	US-11-217-529-3039	Sequence 3039, Ap
c 5	14.6	69.5	1009	6	US-10-953-349-3661	Sequence 3661, Ap
c 6	14.6	69.5	1850	6	US-10-953-349-16973	Sequence 16973, A
7	14.6	69.5	2316	7	US-11-217-529-5833	Sequence 5833, Ap
8	14.6	69.5	4434	7	US-11-217-529-76875	Sequence 76875, A
9	14.4	68.6	1355	6	US-10-953-349-25095	Sequence 25095, A
10	14.4	68.6	3414	7	US-11-217-529-79249	Sequence 79249, A
11	14.2	67.6	423	7	US-11-217-529-79945	Sequence 79945, A
c 12	14.2	67.6	449	6	US-10-473-173-445	Sequence 445, App
c 13	14.2	67.6	576	6	US-10-953-349-7850	Sequence 7850, Ap
14	14.2	67.6	900	6	US-10-953-349-24207	Sequence 24207, A

	15	14.2	67.6	960	7	US-11-121-154-78	Sequence 78, Appl
	16	14.2	67.6	1403	6	US-10-953-349-31669	Sequence 31669, A
	17	14.2	67.6	1638	7	US-11-217-529-5647	Sequence 5647, Ap
	18	14.2	67.6	1756	6	US-10-953-349-22761	Sequence 22761, A
c	19	14.2	67.6	1789	7	US-11-293-697-1953	Sequence 1953, Ap
	20	14.2	67.6	3075	7	US-11-217-529-77428	Sequence 77428, A
c	21	14.2	67.6	5920	7	US-11-145-307A-185	Sequence 185, App
	22	13.8	65.7	555	7	US-11-217-529-1715	Sequence 1715, Ap
	23	13.8	65.7	946	6	US-10-953-349-9605	Sequence 9605, Ap
	24	13.8	65.7	981	7	US-11-217-529-5653	Sequence 5653, Ap
c	25	13.8	65.7	1314	6	US-10-953-349-33472	Sequence 33472, A
	26	13.8	65.7	1932	6	US-10-953-349-36403	Sequence 36403, A
c	27	13.8	65.7	1938	7	US-11-217-529-3079	Sequence 3079, Ap
c	28	13.8	65.7	2098	7	US-11-242-111-10	Sequence 10, Appl
c	29	13.8	65.7	2140	6	US-10-505-928-707	Sequence 707, App
	30	13.8	65.7	2575	7	US-11-293-697-736	Sequence 736, App
	31	13.8	65.7	4695	7	US-11-217-529-80934	Sequence 80934, A
	32	13.6	64.8	738	7	US-11-217-529-77329	Sequence 77329, A
	33	13.6	64.8	1029	7	US-11-217-529-3359	

GenCore version 5.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 04:39:39 ; Search time 454.588 Seconds  
 (without alignments)  
 2583.230 Million cell updates/sec

Title: US-10-718-955-8  
 Perfect score: 21  
 Sequence: 1 cgatttaaggggcaagtttagc 21

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

Database : EST:\*  
 1: gb\_est1:\*  
 2: gb\_est3:\*  
 3: gb\_est4:\*  
 4: gb\_est5:\*  
 5: gb\_est6:\*  
 6: gb\_htc:\*  
 7: gb\_est2:\*  
 8: gb\_est7:\*  
 9: gb\_est8:\*  
 10: gb\_est9:\*  
 11: gb\_gss1:\*  
 12: gb\_gss2:\*  
 13: gb\_gss3:\*  
 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	18.4	87.6	129	7	AW897451	AW897451 CM0-NN005
	2	17.8	84.8	660	14	DX135569	DX135569 OG_ABa016
c	3	17.8	84.8	1082	12	CC284824	CC284824 CH261-188
c	4	17.4	82.9	232	2	BG885153	BG885153 dac36h12.
c	5	17.4	82.9	435	9	DN168287	DN168287 LH_Ea03B
	6	17.4	82.9	699	11	BH954275	BH954275 odi84e07.
c	7	17.4	82.9	727	14	AG431543	AG431543 Mus muscu
c	8	17.4	82.9	940	14	DU741343	DU741343 APKI660.b

c	9	17	81.0	616	7	AV780588	AV780588 AV780588
	10	17	81.0	845	13	CW516526	CW516526 OP__Ba004
c	11	16.8	80.0	297	8	CV623541	CV623541 L_AH-aaa2
	12	16.8	80.0	347	4	BY145940	BY145940 BY145940
	13	16.8	80.0	352	4	BY137858	BY137858 BY137858
	14	16.8	80.0	353	4	BY782356	BY782356 BY782356
	15	16.8	80.0	355	4	BY775556	BY775556 BY775556
	16	16.8	80.0	358	4	BY788876	BY788876 BY788876
	17	16.8	80.0	368	4	BY131922	BY131922 BY131922
	18	16.8	80.0	368	4	BY773684	BY773684 BY773684
	19	16.8	80.0	370	4	BY766589	BY766589 BY766589
	20	16.8	80.0	392	5	CD702231	CD702231 EST18755
	21	16.8	80.0	412	1	AI891127	AI891127 wn28h06.x
c	22	16.8	80.0	434	7	BE800557	BE800557 sq94h05.y
c	23	16.8	80.0	434	11	BH304351	BH304351 CH230-200
	24	16.8	80.0	499	7	BB706398	BB706398 BB706398
c	25	16.8	80.0	527	12	CC171791	CC171791 ii74a04.b
	26	16.8	80.0	558	1	AA259935	AA259935 va53c07.r
c	27	16.8	80.0	569	5	CD564766	CD564766 B0484D06-
	28	16.8	80.0	581	14	DE132931	DE132931 Oryzias 1
	29	16.8	80.0	594	10	DY062349	DY062349 001118BAM
	30	16.8	80.0	607	7	BB638944	BB638944 BB638944
	31	16.8	80.0	621	5	CK327581	CK327581 EST4891 Z
	32	16.8	80.0	624	7	BB660123	BB660123 BB660123
	33	16.8	80.0	633	7	BB612365	BB612365 BB612365
	34	16.8	80.0	636	13	CZ313318	CZ313318 ZMMBF0011
	35	16.8	80.0	641	5	CK758061	CK758061 eca01-8cs
	36	16.8	80.0	649	7	BF045761	BF045761 BP250013B
	37	16.8	80.0	651	9	DN369676	DN369676 LIB3731-0
c	38	16.8	80.0	657	11	BH335239	BH335239 CH230-5D1
	39	16.8	80.0	658	4	BY740523	BY740523 BY740523
	40	16.8	80.0	668	3	BU281515	BU281515 603864010
	41	16.8	80.0	680	7	BB627337	BB627337 BB627337
c	42	16.8	80.0	684	13	CW782340	CW782340 OP__Ba007
	43	16.8	80.0	718	7	BB628501	BB628501 BB628501
c	44	16.8	80.0	726	8	CX229538	CX229538 MBM04366
	45	16.8	80.0	728	13	CZ116285	CZ116285 OA_BB000
	46	16.8	80.0	735	14	DE132933	DE132933 Oryzias 1
	47	16.8	80.0	753	4	BY709485	BY709485 BY709485
	48	16.8	80.0	787	3	BU425942	BU425942

GenCore version 5.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 04:56:26 ; Search time 268.82 Seconds  
 (without alignments)  
 1955.884 Million cell updates/sec

Title: US-10-718-955-1  
 Perfect score: 281  
 Sequence: 1 gtgagaaaacactctttcct.....tgccccttaaatacgctccag 281

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 600 summaries

Database : Issued\_Patents\_NA:\*  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*  
 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	65.6	23.3	194937	3	US-09-949-016-17032	Sequence 17032, A
2	65.6	23.3	194937	3	US-09-949-016-17033	Sequence 17033, A
c 3	65.4	23.3	601	3	US-09-949-016-198482	Sequence 198482,
c 4	64.2	22.8	601	3	US-09-949-016-198483	Sequence 198483,
c 5	64.2	22.8	601	3	US-09-949-016-198484	Sequence 198484,
6	64.2	22.8	767677	3	US-09-949-016-12147	Sequence 12147, A
7	64.2	22.8	767677	3	US-09-949-016-17361	Sequence 17361, A
c 8	63.8	22.7	601	3	US-09-949-016-198480	Sequence 198480,
c 9	63.8	22.7	601	3	US-09-949-016-198481	Sequence 198481,
c 10	63.4	22.6	16434	3	US-09-949-016-13235	Sequence 13235, A
c 11	63.4	22.6	26831	3	US-09-949-016-16250	Sequence 16250, A
12	61	21.7	6727	3	US-08-629-643A-5	Sequence 5, Appli

	13	61	21.7	6727	3	US-09-280-799-1	Sequence 1, Appli
	14	61	21.7	6727	3	US-09-155-884-5	Sequence 5, Appli
c	15	60.8	21.6	36221	3	US-09-954-556-29	Sequence 29, Appl
	16	60.8	21.6	670689	3	US-09-949-016-12505	Sequence 12505, A
	17	60.8	21.6	670690	3	US-09-949-016-14207	Sequence 14207, A
	18	59.4	21.1	112114	3	US-09-949-016-17292	Sequence 17292, A
	19	59.4	21.1	154605	3	US-09-949-016-11894	Sequence 11894, A
	20	59	21.0	2551	2	US-08-486-013-70	Sequence 70, Appl
	21	59	21.0	2551	2	US-08-482-279-70	Sequence 70, Appl
	22	59	21.0	2551	2	US-08-342-268-70	Sequence 70, Appl
	23	59	21.0	2551	3	US-09-015-968-70	Sequence 70, Appl
	24	59	21.0	2551	3	US-09-397-386-70	Sequence 70, Appl
c	25	58.2	20.7	12645	3	US-09-949-016-12306	Sequence 12306, A
	26	58	20.6	601	3	US-09-949-016-57873	Sequence 57873, A
	27	58	20.6	72048	3	US-09-949-002-600	Sequence 600, App
	28	58	20.6	72048	3	US-09-949-002-684	Sequence 684, App
	29	57.6	20.5	601	3	US-09-949-002-5378	Sequence 5378, Ap
	30	57.4	20.4	87648	3	US-09-949-016-13655	Sequence 13655, A
	31	57.2	20.4	304533	3	US-09-949-016-15371	Sequence 15371, A
	32	57.2	20.4	304533	3	US-09-949-016-15372	Sequence 15372, A
	33	57	20.3	601	3	US-09-949-016-31837	Sequence 31837, A
	34	57	20.3	601	3	US-09-949-016-40022	Sequence 40022, A
	35	57	20.3	601	3	US-09-949-016-74004	Sequence 74004, A
	36	57	20.3	601	3	US-09-949-016-74110	Sequence 74110, A
	37	57	20.3	1016	2	US-08-109-391A-3	Sequence 3, Appli
	38	57	20.3	1016	2	US-08-459-019A-3	Sequence 3, Appli
	39	57	20.3	1016	2	US-08-460-428A-3	Sequence 3, Appli
	40	57	20.3	1016	3	US-08-458-860A-3	Sequence 3, Appli
	41	57	20.3	1016	3	US-09-196-447B-3	Sequence 3, Appli
c	42	57	20.3	69813	3	US-09-949-016-12455	Sequence 12455, A
c	43	57	20.3	69813	3	US-09-949-016-13905	Sequence 13905, A
c	44	57	20.3	69813	3	US-09-949-016-13906	Sequence 13906, A
c	45	57	20.3	69833	3	US-09-949-016-12861	Sequence 12861, A
	46	56.8	20.2	601	3	US-09-949-016-57872	Sequence 57872, A
	47	56.8	20.2	236474	3	US-09-949-016-13418	Sequence 13418, A
c	48	56.6	20.1	4084	3	US-08-866-340-1	Sequence 1, Appli
c	49	56.6	20.1	4460	3	US-09-103-875-4	Sequence 4, Appli
	50	56.4	20.1	601	3	US-09-949-002-5377	Sequence 5377, Ap